# ABORTIVE T5 BACTERIOPHAGE INFECTIONS OF Escherichia coli CONTAINING THE COLICINOGENIC FACTOR, Collb

Bv

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To Steven E. Ross and the late James W. Dunlop – Their accomplishments have given me inspiration, and their advice and encouragement have given me direction.

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#### ABBREVIATIONS USED

-- α-methylglucoside (α-methyl-D-glucopyranoside) αMG

-- N,N'-dicyclohexylcarbodiimide DCCD

EDTA -- ethylenediamine tetraacetate

NPN -- N-phenyl-1-naphthylamine

-- o-nitrophenylgalactoside ONPG

SDS -- sodium dodecvl sulfate -- simian virus 4D

TCA -- trichloroacetic acid

SV4D

TEMED -- N.N.N'.N'-tetra-methyl-ethylenediamine

TES buffer -- Tris-EDTA-saline buffer

-- thio-β-methyl-D-galactoside TMG

Abstract of Dissertation Presented to the Graduate Council of the University of Florida in Partial Fulfillment of the Requirements for the Degree of Doctor of Philosophy

# ABORTIVE T5 BACTERIOPHAGE INFECTIONS OF Escherichia coli CONTAINING THE COLICINOGENIC FACTOR, Colib

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When bacteriophage T5 infect Escherichia coli containing the colicinogenic factor, Collb, the infections are abortive. RNA and protein syntheses stop abruptly and simultaneously at about 12 minutes after adsprotion, and no progeny phage are produced. In the current work. I have shown that numerous changes in membrane function appear at nearly the same time as cessation of macromolecular syntheses. These alterations include inhibition of glutamine and proline uptake, stimulation of a-methylglucoside uptake, increased fluorescence intensity emitted by a membrane-binding probe, and efflux of preloaded potassium ions. The combination of results suggests that the infectious process is halted because of membrane depolarization. The same pattern of pathophysiological changes occurs during infections of Collh<sup>+</sup> hosts by T5 mutants deficient in second-step transfer of DNA, indicating that no early or late phage gene expression is necessary to elicit the abortive response.

#### INTRODUCTION

Extrachromosomal elements of bacteria carry from cell to cell a tremendous variety of genetic determinants. At least 30 types of lysogenized phage are found among coliforms (26), and over 250 kinds of plasmids are established in <u>F. coli</u> alone (63). Actually, such figures might grossly underestimate the true numbers, since modifications and rearrangements of nucleotide sequences within any single cell probably continuously yield new genetic combinations (22,89). These novel structures efficiently pass to other bactera — even to unrelated bacteria. Then, the process is repeated, implementing rapid change in the genetic complement of bacterial populations.

Extrachromosomal elements are eminently suited, therefore, to serve as instruments for bacterial adoptation, and they do in fact often provide strong survival advantage to the cells in which they reside (89). In certain Enterbacterial strains, for example, some types of extrachromosomal elements enable their hosts to prevent replication of particular virulent bacteriophages. This can be accomplished in several ways. Some elements carry genetic determinants that alter specific viral receptors, making the cell resistant to the phage which normally adsorb to that site (1). Another mechanism is superinfection exclusion (2,3,31). Here, adsorption is normal. This term describes the ability of one phage --- the extrachromosomal element in this case --- to prevent entry of DNA from a second phage that is subsequently adsorbed. The genome of the

superinfecting virus is trapped within the cell envelope, preventing any phage gene expression. Yet another way that some genetic elements circumvent viral replication is by directing the synthesis of restriction endonucleases (72). These enzymes break down incoming DNA that is unmodified at specific restriction sites. Finally, there is abortive infection, during which adsorption and DNA entry are normal, and the viral genome remains intact. The initial stages of viral gene expression occur as usual, but the presence of a lysogenized phage or a plasmid in some way prevents the infecting virus from producing propoeny.

Of these four mechanisms -- resistance, superinfection exclusion, restriction, and abortive infection -- abortive infection remains the least understood. This is the case despite extensive study of several abortive systems, among which are T7 infections of F (fertility factor)-containing <u>E</u>. colf (11,12,13,23,24,66,76), T-even rII mutant infections of  $\lambda$  lysogens (14,34,39,32), and T-even or T5 infections of P2 lysogens (8,9,10,35).

The long-term objective of my research is to elucidate the mechanism underlying the abortive infection which occurs after T5, or its close relative BF23, infects <u>E</u>. <u>coll</u> containing the colicinogenic factor, Collb. Studies described herein answer several questions that are important steps toward realizing this goal.

Abortive Infections Mediated by the Collb Factor

Strains of  $\underline{E}$ .  $\underline{coli}$  carrying the colicinogenic factor, Collb, are nonpermissive hosts for bacteriophage BF23 (80,97). However, bacteria containing the F-factor, the  $\lambda$  prophage, or the Pl prophage are able

to support replication of this phage. Likewise, BF23 can replicate in the presence of ColB, ColV, ColE1-30, ColE2-P9, and Colla. Thus, the viral infection is not aborted because of the presence of extra-chromosomal DMA in general; rather, specific genetic determinants on the plasmid are involved.

It is not surprising that TS shares BF23's inability to grow in Collb-containing cells (80). This characteristic is just one of many the two phages have in common (reviewed in 87). They also have collnear maps and undergo phenotypic mixing, gene product substitution, and genetic recombination.

Productive BF23 and T5 infections are very similar as well. Both viruses are unusual in that they inject their genomes in two steps (59,60,61,62). The first-step-transfer DNA, constituting only 8% of the whole, codes exclusively for class I (pre-early) proteins (70). These proteins are synthesized from about 1 minute until about 10 minutes after infection. One of them, the Al gene product, is required for host DNA degradation (62,71). The Al polypeptide and also the A2 gene product are required for entry of the remaining second-step-transfer DNA. Carrying all class II (early) and class III (late) genes, the other 92% of the genome enters the host at about 4 minutes after infection, several minutes before early protein synthesis begins (70). The early proteins are necessary for phage DNA replication, which begins about 9 minutes into the infectious process (25). Late proteins, the structural proteins included, first appear at about 13 minutes and are synthesized until lysis, approximately 1 hour after infection (70).

Abortive infections begin in the same way, but become manifestly abnormal after a short time (79). Phage ONA entry occurs normally, and the infecting genome remains intact (79,97). Pre-early gene expression proceeds as usual, resulting in degradation of the bacterial genome and death of the host cell. Then, at about 8 to 12 minutes after adsorption, incorporation of RNA and protein precursors into macromolecules stops. Little early protein synthesis occurs, and no late proteins appear. Since early proteins are required for phage ONA synthesis (69), it is not surprising that phage ONA replication is prevented. Finally, some laboratories observe rapid cell lysis of infected nonpermissive cells 15 to 30 minutes after phage protein synthesis begins (80).

A few phage circumvent the abortive process, producing plaques at an efficiency of plating about 10<sup>-6</sup> relative to that on noncolicinogenic hosts (74,80). These host-range [n] mutants, which are recessive to wild-type in mixed infections, have a mutation in a pre-early gene (5,74). In 15, the mutation lies in gene A3, and the mutants fail to produce a small protein with a molecular weight of 12,000 (98). The T5 A3 gene product is thought to be identical to PES seen on polyacrylamide gels after electrophoresis of infected-cell extracts (0. J. McCorquodale, personal communication). Similarly, BEZ3 host-range mutants have a mutation in gene P3 (corresponding to A3 of T5 on the colinear maps). Furthermore, the electrophoretic mobility of PES derived from cells infected with BF23 h<sup>-</sup> mutants is altered, consistent with the suggestion that PES is the P3 gene product. Hence, it appears that the A3 or P3 gene product must be present to elicit the abortive response.

It has been proposed that early protein synthesis is required in abortive T5 infections (45). It had been shown that if T5 infects cells in the presence of very low calcium concentrations, only preearly proteins are expressed (77,78). When additional calcium is added later, however, early RNA and proteins quickly appear. If Collb<sup>+</sup> hosts are infected with T5 in the presence of little calcium, allowed to synthesize only pre-early proteins for 12 minutes, then supplemented with additional calcium, RNA synthesis proceeds for only a short time thereafter; i.e., the infection aborts soon after calcium supplementation (45). If the same experiment is performed, except that chloramphenicol is added just prior to calcium addition, RNA synthesis continues much longer than when chloramphenical is not added. The implication is that chloramphenicol, in the second case, prevents synthesis of an early protein(s) necessary for activating the abortive mechanism. At least one alternative explanation, however, is that a low calcium concentration present at the time of infection might also slow production of pre-early proteins (69). This could be expected to inhibit production of the A3 gene product and might delay cessation of macromolecular synthesis.

To determine if any early protein synthesis is indeed necessary to halt the infectious process, I have taken another approach using TSAI mutants. Because a functional Al protein is lacking, these phage can synthesize only pre-early proteins; second-step DNA transfer does not occur (62,71). I will show here that the abortive response appears despite the absence of early proteins, suggesting that the only viral protein required in TS abortive infection is the A3 gene product.

In addition to the phage's own contribution, host-determined factors are involved in abortive infection. One-step growth curves indicate that roughly 5% of the cells in a Collb\* population will support phage replication, though the phage yield per infective center is decreased by 70-85% (75,80). Since the phage that do manage to grow do not grow well upon reinfection of Collb-containing cells, these phages are not host-range mutants; rather, their growth depends on a low level of permissiveness in a few cells among the host population. The degree of T5 inhibition is also dependent to some extent upon the particular host strain carrying the plasmid (79). For example, the yield of T5 infectious centers on E. coli M3110 (Collb) is similar to that if T5 is grown on M3110 polA] (Collb). The average phage yield per infective center, however, is 5-fold greater on the strain with normal ability to produce host ONA polymerase i.

Furthermore, some Collb-containing strains are permissive because of mutations on chromosomal or plasmid DIM (50,69, Richard Moyer, personal communication). Genetic analysis of these strains reveals that mutations at two chromosomal loci are necessary to express a fully permissive phenotype. The first locus, designated <a href="mailto:cmm4">cmm4</a>
(Collb-mediated resistance) on the <a href="mailto:c.coll">c.coll</a> map, is 91% cotransducible with <a href="mailto:rspE">rspE</a> and is proximal to <a href="mailto:aroE">aroE</a>. The second, <a href="mailto:cmmB">cmmB</a>, is 75% cotransducible with <a href="mailto:rspE">rspE</a> and is distal to <a href="mailto:aroE">aroE</a>. Other strains are permissive because of plasmid-borne mutations, but these have not been mapped. Thus, taken together, the studies indicate that contributions by plasmid, host, and phage are all necessary to produce an abortive infection.

To determine how the various factors interact to arrest the infection is a complex problem. It had been hypothesized that the primary defect is in transcription (79). Fully active RNA polymerase is recoverable from infected Collb-containing cells, however, indicating that this enzyme is not the target (99). Alterations of the DNA template have also been studied to see if there are any which could explain cessation of gene expression. Packaged DNA is nicked, but the genome is ligated soon after infection (45). Only in productive infections, however, is the DNA subsequently renicked, suggesting that the transcriptional program during abortive infection could be altered as a result. Since ligated DNA is transcribed normally in an <u>in vitro</u> system (54), though, the relevance of the finding is questionable. A direct approach would be to determine if DNA extracted from abortively infected cells can direct <u>in vitro</u> transcription, but this has not been done.

It has also been proposed that the primary defect is at the translational level (SD). The <u>cmrA</u> locus maps near the gene coding for a ribosomal protein. This suggests that the ribosomal apparatus might be implicated, but no study has determined if extracts from abortively infected cells can support in <u>vitro</u> translation. Thus, while no sound basis for a primary transcriptional or translational defect has been found, the studies looking for such abnormalities have not been exhaustive and cannot, therefore, rule out these possibilities.

Since it has previously been hypothesized that membrane dysfunction causes the abortion of T7 infections of male E. coli (12,23) and of T-even rII mutant infections of  $\lambda$  lysogens (34,39), another line of investigation has been to examine changes in the cell envelope during abortive 15 infection. Infected nonpermissive cells become tensitive to sodium dodecyl sulfate (SDS)-induced lysis, unlike their infected Collb counterparts (19). Although indicative of structural alterations in the host's outer membrane which allows the detergent to reach the inner membrane, this change occurs later than the cessation of macromolecular synthesis. As mentioned previously, some laboratories also note early abortive lysis (80), but the meaning of this event is not clear either. No progeny phage are produced even when premature lysis is prevented by stabilizing the host cells in medium of high osmolarity. Furthermore, our laboratory does not observe the spontaneous lysis (19).

I have looked more closely at membrane function during T5 infections of Collb<sup>+</sup> hosts to determine if physiological alterations of the membrane could possibly account for the abortive response. The results suggest that host membrane depolarization is the primary event leading to cessation of the T5 infectious process.

#### MATERIALS AND METHODS

# Organisms

The bacterial strains used for most experiments are characterized in Table 1. Richard Moyer supplied our laboratory with theretrains which are isogenic. RM 42 contains no plasmid; RM 43 bears wild-type Collb-P9; RM 39 has a murant Collb plasmid which renders the host permissive for T5 (Richard Moyer, personal communication). Other strains were occasionally used, as indicated. E. coll was originally obtained from M. J. Bessman and maintained for many years in Donna Duckworth's laboratory, whereas E. coll CHF4704) was taken from a stock maintained by Milliam Holloman. E. coll CRG3 was the gift of M. L. Dirksen.

Rolf Benzinger provided wild-type bacteriophage T5; T5hl2<sup>-</sup>,
T5an16d, and T5anH27 were obtained from D. J. McCorquodale. Relative
plating efficiencies of the phage stocks on the various bacterial
strains are also shown in Table 1. T5hl2<sup>-</sup> has a mutation which
allows it to replicate in Collb<sup>+</sup> cells (74), whereas T5anl6d and
T5anlH27 each have an amber mutation in the Al gene (5).

# Media and Growth of Bacteria

The growth medium used for most experiments was M9 phosphate-buffered, balanced salt solution (46), supplemented with glucose (0.53), veast extract (0.05%),  $CaCl_2$  (5 x  $10^{-4}$  M), and thymine (50 $\omega$ g per m1). Other additives were present as indicated in the description of each experiment. Unless otherwise indicated, bacteria were grown from a

TABLE 1. Characterization of Bacteria and Phage

(sn <sub>+</sub> )	T5amH27	10-5	6-01>	10-5 10-5	
ive to CR63	TSaml6d	10-5 10-5	6-01> 6-01>	9-01	
cy Relati	T5h12"	-	0.5	е	į
Plating Efficiency Relative to CR63(su <sup>+</sup> )	TS Wild-type(T5wt) T5hl2 T5aml6d T5amH27	-	10-7	-	
Caliata	Production		+	+	
	Genotype	W3110 (thy-, ColI <sup>R1</sup> )	W3110 (thy-, Coll <sup>R</sup> , Collb-P9)	W3110 (thy <sup>-</sup> , ColIR, Collb-P9h <sup>-2</sup> )	
F. coli	Strain	RM 42	RM 43	RM 39	

<sup>2</sup>Collb-P9h indicates a mutant Collb factor which allows T5 replication.  $^{1}\text{Coll}^{R}$  indicated resistance to the external action of Colicin Ib.

5% inoculum of an overnight culture. Growth was followed by monitoring turbidity on a Klett-Summerson colorimeter (660 nm filter), which had been previously calibrated to numbers of bacterial colony formers.

Potassum efflux experiments were performed using dilute tryptone broth (4 g tryptone and 2.5 g NaCl per liter of medium) as growth medium. Hershey broth (8 g of nutrient broth, 5 g of peptone, 5 g of NaCl per liter) was employed for some purposes, where indicated. Growth in these media was followed in the manner outlined above.

Finally, Tris-buffered medium was used. Per liter, this medium contains 2.0 g of NH $_{2}$ (1, 5.0 g of NaC1, 0.4 g of KC1, 0.01 g of NgC1 $_{2}$ -6HgO, 0.22 g of Na $_{2}$ SO $_{4}$ , 5.0 g of Casamino acids, 2.5 ml of 80% glycerol, 250 mg of thiamine, and 100 ml of Tris (1 M, pH 7.3).

## Colicin Production

To determine if a particular bacterial strain produced a colicin, I used the method of Fredericq (38). The cells were grown in Hershey broth for 48 hours. Then, chloroform (1%) was added, and the suspension was agitated for 10 seconds. Thereafter, the suspension was centrifuged at 10,000 rpm for 10 minutes on an SS-34 rotor in a Sorvall (RC-5). The supernatant (0.005 ml) was spotted on sensitive indicator lawns of  $\underline{E}$ ,  $\underline{col}$ 1 & and  $\underline{E}$ ,  $\underline{col}$ 1 C. If a zone of clearing appeared after overmight incubation of the plates, the strain was called a colicinovoducer. Results are indicated in Table 1.

# Phage Growth

Phage stocks were prepared in one of two ways: by the confluent lysis technique of Adams (1), or by recovering phage from Hershey broth by polyethylene glycol precipitation (105). No differences in results were obtained using the different types of phage preparation.

#### Phage Infections

Bacterial hosts were grown, as outlined above, to a concentration of approximately 6 x  $10^8$  cells per ml. The bacteria were then centrifuged at  $4^6$ C for 10 minutes at 10,000 rpm in an SS-34 rotor on Sorvall (RC-5), and resuspended in 1/10th volume of fresh growth medium. Phage were added at a multiplicity of infection of 10 (except where indicated otherwise), and after 1 minute, the bacteria-virus mixture was rediluted in prevarmed growth medium to  $6 \times 10^8$  cells per ml. The time of redilution was called time zero.

# Macromolecular Synthesis

RNA synthesis was monitored by measuring incorporation of  $[^3h]$ -uridine into acid-insoluble material at different times after infection. Bacteria were grown in basic growth medium, with 50 µg of uridine added per ml of medium. Bacteria were centrifuged, diluted, infected, and rediluted as outlined above. At time zero,  $[^3h]$  uridine (1 µtilor of the per ml, 5 µtilor per µmole) was added and, at indicated intervals thereafter, 0.9 ml aliquots were removed and added to 0.1 ml of cold 50% trichloroacetic acid (TCA). Of this mixture, 0.4 ml was filtered through Whatman glass fiber filters (GF/F) and washed with 15 ml of cold 5% TCA. The filters were dried in an oven at 60°C for about 1 hour, and counted in a toluene-based liquid scintillation fluid using a Beckman LS200 counter. The results represent total (cumulative) counts per minute incorporated into samples of approximately 2.2 x  $10^6$  bacteria.

Protein synthesis was measured in the same way, except that amino acids were used. When tyrosine was employed, cold tyrosine  $(25~\mu g~per~ml)$  was added to basic growth medium, and  $f^3 Hl^2$  tyrosine

(1  $\mu$ Cf per m1, 7.2  $\mu$ Cf per  $\mu$ mole) was added at time zero. When proline incorporation was measured, cold proline (25  $\mu$ g per m1) was added to basic growth medium, and  $\Gamma^2$ M1) proline (1  $\mu$ Cf per m1, 4.8  $\mu$ Cf per  $\mu$ mole) was added at time zero. Experiments to measure incorporation of glucose were also performed as above, adding  $\Gamma^4$ Cf glucose (0.5  $\mu$ Cf per m1, 0.1  $\mu$ Cf per  $\mu$ mole) at time zero.

Scintillation fluid consisted to toluene (1 gallon), 19 g of PPO (2,5-diphenyloxazole), and 1,14 g of PPOP [1,4-bis-(5-phenyloxazoyl)) benzen]. A magnetic stirring bar agitated a newly made mixture over-night.

#### Dye-Buoyant Density Equilibrium Centrifugation of Bacterial DNA

Bacterial DNA was labeled, extracted, and banded on ethidium bromide-cesium chloride gradients according to a modification of the method of Clewell and Helinski (20,21).

Tris-buffered growth medium was used to grow bacteria from a 1:100 dilution of an overnight culture until the turbidity reached 115 Klett units (660 m filter). RM 42 and RM 39 were grown in 15 ml of medium, whereas 30 ml of an RM 43 culture was grown. RM 42 and RM 39 were incubated in the presence of [<sup>14</sup>C] thymidine (50 µCi per ml, 1 µCi per 4 µg of thymidine); [<sup>3</sup>Nl] thymidine (50 µCi per ml, 1 µCi per 4 µg of thymidine); [<sup>3</sup>Nl] thymidine (50 µCi per ml, 1 µCi per 4 µg of thymidine) was used to label RM 43 DNN. After cells had reached the desired concentration, 15 ml of the RM 42 culture was mixed with 15 ml of the RM 43 culture, and 15 ml of the RM 34 culture was mixed with 15 ml of the RM 43 culture.

Each tube, containing a total of 30 ml of bacterial suspension, was spun at 10,000 rpm in an SS-34 rotor in a Sorvall (RC-5). Each

pellet was resuspended in 1 ml of cold 25% sucrose in Tris (0.05 M, pH 8). Lysozyme (0.2 ml of a solution, 5 mg per ml in Tris [0.25 M, pH 8]) was added, and the suspension was maintained at 0°C for 5 minutes. Thereafter, ethylenediamine tetraacetate (EUTA) (0.4 ml of an aqueous solution, 0.25 M adjusted to pH 8) was added subsequently and, with occasional swirling, maintained for another 5 minutes at 0°C. Then, 1.6 ml of a detergent solution (1% Brij 58, 0.4% sodium deoxycholate, 0.0625 M EOTA, 0.05 M Tris, pH 8) was added to the suspension, and the mixture was maintained at 0°C until cell lysis, 3 to 5 minutes later. The lysate was spun at 2°C for 25 minutes at 20,000 rpm in an SS-34 rotor on a Sorvall (RC-5). The supernatant should only contain about 5% of the original quantity of chromosomal ONA and is called the cleared lysate.

Each of the cleared lysates was diluted to 12 ml in TES buffer (0.05 M NaCl, 0.005 M EOTA, 0.03 M Tris, pH 8), and 3 ml of an ethidium bromide solution (1 mg of ethidium bromide in 1 ml of TES buffer) was added. Then, CsCl was added in a quantity sufficient to bring the refractive index to 1.3896. Each mixture was spun in a Ti-60 fixed angle rotor at 22,000 rmm at 4°C for 60 hours.

An 18 guage needle was inserted into the bottom of each centriuge tube, and 0.25 ml samples were recovered. The refractive index of representative samples was determined. Each sample was then mixed with 0.05 ml of 50% trichloroacetic acid, and 0.15 ml of this mixture was filtered over Mhatman glass fiber filters (GF/F). Each filter was washed with 15 ml of 5% TCA, placed in a glass vial, and dried in an oven at 60°C for 1 hour. A toluene-based scintillation fluor was added (5 ml in each vial), and the scintillations per minute were determined on a Beckman LS200 counter using the narrow  $[^3{\rm H}]{\text{-window}}$  and the  $[^{14}{\rm C}]{\text{-window}}$  purchased from Beckman.

# Host-Cell DNA Breakdown

Bacteria were grown as previously described in basic growth medium (defined above) modified by having thymidine (25 µg per ml) in place of thymine. The medium also contained [ $^2$ H] thymidine (0.4 µCi per ml; 1 µCi per 50 µg of thymidine). When the cells reached the appropriate concentration, they were spun, washed twice in medium without labeled thymidine, concentrated, infected, and rediffued as described previously. Thereafter, 0.9 ml samples were removed at the indicated intervals and were added to 0.1 ml of 50% cold TCA. Of this, 0.4 ml samples were filtered over limbatum glass fiber filters (GF/C) and washed with 15 ml of 5% TCA. The filters were placed in glass vials and dried for 1 hour in an oven at 60°C. Scintillations per minute in a toluene-based liquid scintillation fluid were counted on a Beckman LS200 counter.

# Proline and Glutamine Uptake

In these experiments, the amount of amino acid taken up by the cell in a 30-, 60-, or 90-second pulse is measured at various times after infection. Bacteria were grown in basic growth medium, spun, concentrated, infected, and rediluted as above. At the indicated times, 2 ml samples were removed, and chloramphenicol was added, yielding a final concentration of 100 µg per ml. One minute later, 0.9 ml of this mixture was added to 0.1 ml of the labeled amino acid solution. In the proline assay, 1 µci [3] proline (25 µci per µmole) was present, while in the glutamine experiments, 0.5 µci of

[14c] glutamine (5 µCi per µmole) was present. At indicated intervals after infected becteria were added to the labeled amino acid, 0.4 ml samples were removed, filtered on Whatman glass fiber filters (GF/F), and washed with 8 ml of M9. A positive control was done using uninfected cells; a negative control was done using cells treated for 15 minutes with NaM<sub>3</sub> (1%) prior to addition of chloramphenicol. The results are presented here as percentage of uptake in infected cells, relative to that of uninfected controls.

# α-Methylglucoside (αMG) Uptake

 $\alpha$ -Methylglucoside uptake experiments utilized bacteria grown and infected in basic growth medium, as outlined above. At times indicated, I ml of the sample was removed and spun in an Eppendorf 3200 Centrifuge for approximately 30 seconds, resuspended in an equal volume of M9, and spun again. After the second spin, the bacteria were resuspended in basic growth medium, modified by having only 18  $\mu$ g glucose per ml of medium. Of this suspension, 0.9 ml was added to 0.1 ml of  $\Gamma^{14}\mathrm{Cl}$  MG solution (1  $\mu$ Ci per ml, 184  $\nu$ Ci per mole). At indicated intervals, 0.4 ml aliquous were removed and filtered over Mattnan glass fiber filters (GF/F) and washed with 8 ml of M9. The filters were dried and counted. A positive uninfected control was done; a negative control was done using cells treated for 15 minutes prior to the assay with NaF (0.07 M) and NaN<sub>3</sub> (1%). The results are presented as percentage of uptake, relative to uninfected controls.

## Fluorescence Experiments

Fluorescence intensity was measured using a Perkin-Elmer MPF-2A scanning fluorimeter equipped with a temperature-controlled chamber. The instrument's output was corrected for wavelength variable response by means of a rhodamine B quantum counter, and its monochromators were calibrated against the xenon line emission spectrum.

From recrystallized N-phenyl-1-naphthylamine (NPN) a working stock (20 mM in methanol) was prepared. Cells were grown, concentrated, and infected as described previously, except that the multiplicity of infection was 5. At time zero, the infected cells were resuspended in prevarmed (37°C) growth medium containing 10 µM NPN. Three milliliter of the infected-cell samples was placed in quartz cuvettes and inserted into the 37°C chamber.

Fluorescence intensity was measured in arbitrary units and recorded over time after infection. Excitation wavelength was 352mm with a bandwidth of 5mm. The emission wavelength was 410nm with a bandwidth of 10mm.

# Potassium Efflux

Dilute tryptone broth was used as growth medium. This medium contains a low concentration of patassium, making it easier to load cells with radiolabeled potassium (94,101).

Batteria were grown for several generations in the presence of 0.1-0.2 mCi of  $^{42}$ K per ml  $^{12}$ K in the form of KCl in aqueous solution, 0.18 mCi per mg K). When the cells reached a concentration of 6 x  $10^{8}$  bacteria per ml, they were spun, concentrated, and infected as usual (a portion of cells was not infected). At intervals, aliquots of uninfected and infected cells were removed, filtered over glass fiber filters (GF/F), and washed with 8 ml of dilute tryptone broth. Cerenkov emissions were counted using the  $[^{34}$ l channel on the Beckman

LS200 counter. The results represent the amount of residual  $^{42}$ K remaining inside infected cells, relative to the amount remaining inside uninfected cells taken at the same time point (expressed as a percentage).

# Attempts to Prevent Abortion of T5 Infection in Collb Hosts

Cells were grown and infected, in 1% tryptone broth with
Tris (5 mM, pH 7.2), as outlined above. Various additives were
present as indicated in Table 7. The final concentrations of the
additives were as follows: (a) potassium, 100 mM (b) magnesium,
80 mM (c) sodium, 80 mM (d) sucrose, 300 mM (e) polyamines, 30 mM.
Others were added in varying amounts, also as indicated in Table 7.
When N,N'-dicyclohexylcarbodifimide (DCCD) was present, it was added
30 minutes prior to phage infection at a concentration of 0.1 mM.
Polyamines, when used, were added at the time of infection. All other
additives were present from the time when a 5% inoculum was added to
fresh medium.

To determine the efficacy of the treatments, a phage titer was determined. Chloroform (1%) was added to the treated cultures 4 to 7 hours after infection, and samples were plated on lawns of <u>E</u>, <u>coll</u> B. This was designed as a screening procedure, so no attempt was made to remove unadsorbed phage.

# Gel Analysis

To see what proteins were labeled with radioactive amino acids after infection, infected cells were pulse-labeled for 5 minutes with  $1 \, \mu {\rm Cl} \ (^{14}{\rm C})$  of an amino acid mixture per ml of culture. The five-minute pulses were initiated at 1, 6, and 11 minutes after infection,

and terminated by the addition of 100 µg of chloramphenicol per ml of medium and by chilling. The cells were then centrifuged, washed two times, and resuspended in 1/10 volume Leamnli electrophorersis buffer (58). The samples were then boiled for 5 minutes. Twenty microliters of each sample was loaded onto a 15% acrylanded slab gel and electrophoresed for 14 hours at 75 volts. The electrode buffer consisted of 0.192 M glycine and 0.1% 505 in 0.025 M Tris, pH 8.3. The dried gel was autoradiographed by exposing it to Kodak XRI film for 10 days.

The gel was prepared by layering a stacking gel over a previously solidified 15% running gel. A stock acrylamide solution contained 30% acrylamide, 0.8% bisacrylamide. The recipe for the stacking gel was as follows: 1.0 ml of the stock acrylamide solution, 2.5 ml of Tris-HC1 (0.5 M, pH 6.8), 6.4 ml of distilled water, 0.1 ml of 10% SDS, 0.04 ml of 20% ammonium persulfate (freshly made), and 0.02 ml of N,N,N',N'-tetra-methyl-ethylenediamine (TEMED). The running gel consisted of the following: 20 ml of stock acrylamide solution. 10 ml of Tris-HCl (1.5 M, pH 8.8), 9.6 ml of distilled water, 0.4 ml of 10% SDS, 0.035 ml of 20% ammonium persulfate (freshly made). 0.01 ml of TEMED. Each type of gel was made by first mixing the acrylamide solution, Tris-HCl, distilled water, and ammonium persulfate. These ingredients were placed in a vacuum flask and held under vacuum for 3 to 5 minutes to degas thoroughly. Thereafter, the SOS and TEMEO were added, the solution was swirled gently, and the gel was poured immediately.

#### Statistical Methods

The means of two sets of data were compared using Student's t-test, according to the method of Snedecor and Cochran (96). When an equal number of data points were included in each set, t values were calculated using the formula:  $t = (\overline{y_1} - \overline{y_2})^{\frac{1}{N}} (\overline{y_1^2} + \overline{y_2^2})^{\frac{1}{N}}$  where  $y_1$  = the mean of data points in set 1, n = the number of data points in each set,  $S_1$  = the standard deviation of the mean for data collected in set 1. P values were derived from a standard table. Application of the t-test presupposes that the data fit a normal t distribution.

# Materials

 $^{42}$ K and the  $\lceil ^{14}$ C]-labeled amino acid mixture were purchased from New England Nuclear, Boston;  $\lceil ^{14}$ C] cMG was purchased from Amersham, Arlington Heights, Illinois. All other radiolabeled products were obtained from Schwarz/Mann, Orangeburg, New York.

APR was the gift of M. A. Cramer of West Lafayette, Indiana.

DCD was purchased from Sigma Chemical Company, St. Louis, Missouri.

All other chemicals used were analytical reagent grade, and are readily available from many producers.

#### RESULTS

# Macromolecular Synthesis in T5 and T5h12 Infections of RM 42, RM 43, and RM 39

It has been previously reported that transcription and translation cease at 6 to 10 minutes after T5 infection of Collion E, Coll (79). To determine when these changes occurred in our system, I measured the cumulative incorporation of an RNA and a protein precursor into acid-insoluble macromolecules at various times after infection. Uridine was used as an indicator of RNA synthesis, while tyrosine or proline was used to monitor protein synthesis. The Colls I have used are described in Table 1, as are the infecting phage.

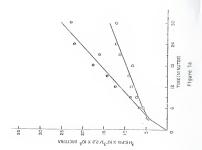
Typical results of experiments measuring incorporation of  $[^2N]$ -uridine can be seen in Figure 1. It can be seen that RMA synthesis, measured in this way, continued for at least 30 minutes in productive infections, albeit at a slower rate than in uninfected cells (Fig. 1a). In infections of RM 43 (Collb), however, uridine incorporation stopped at some time approximately 9 to 12 minutes after initiation of infections (Fig. 1b). Protein synthesis, as indicated by tyrosine or proline incorporation (Fig. 2 and Fig. 3) also stopped about 9 to 12 minutes after infection of Collb-containing cells. RMA and protein synthesis proceeded at least 30 minutes in T5 wild-type infections of RM 33 (Collb) (Fig. 3b).

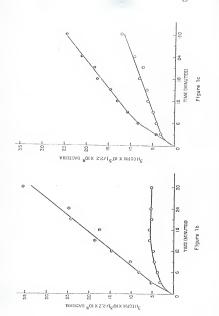
Uridine Incorporation into Acidinsoluble Macromolecules in Uniffected and Infected RM 42, RM 43, and RM 39.

Acid-insoluble material was were removed at the indicated collected on glass fiber filters, and The amount of incorporated radioactivity was determined by liquid-scintillation In Fig. la, the bacteri RM 42, which contain no 1b represents resul obtained with RM 43 (Collb), and Cells were grown and infected in synthetic medium. [3N] Uridine times and mixed with 0.1 filters were washed. 1 µCi per ml, 5 µCi added at time zero. counting. used were 50% TCA. plasmid. 0.9 ml the

Fig. 1c, RM 39 (Collb h<sup>-</sup>)

O, T5-infected cells





Tyrosine Incorporation into Acid-Uninfected and Infected RM 42. insoluble Macromolecules in RM 39. RM 43, and

BACTERIA

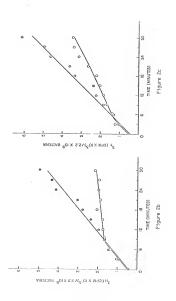
0.9 ml were removed at the indicated cold Samples of Acid-insoluble material Cells were grown and infected in synthetic medium. [3H] Tyrosine (1 µC1 per ml, 7.2 µC1 per umole) recovered on glass fiber fi times and mixed with 0.1 ml of incorporated adioactivity was determined. Fig. 2a, the host was RM Fig. 2b, the host was RM in Fig. 2c, the host was (Collb h<sup>-</sup>). was added at time zero. the amount of 50% TCA. Nas and

<sup>2</sup>H (CP31 X 10<sup>-2</sup>)/S2 X 10<sup>6</sup>

O, T5-infected cells , uninfected cells



3 25 TIME (ACNUTES)

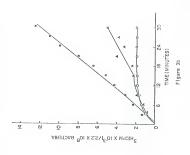


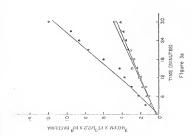
# Proline Incorporation into Acid-Insoluble Macromolecules in Uninfected and Infected RM 42, RM 43, and RM 39. Figure 3.

Coll's were yound in stateful medium. "All postine (1 rif. per mil., 48, 80; per sanis) was deded at time zero. Samples of 0.9 mil were removed at the indicated tries and missed with 0.1 in 0 coll 500; TCD. Acid-friscible materials was recovered on glass fiber filters, and the amount of incorporated relationshipty was determined. In Fig. 3a, the back was 80 43 (colls in).

uninfected cells
 T5-infected cells

▲ , T5hl2<sup>-</sup>-infected cells





### Confirmation that RM 39 Contains Plasmid DNA

RM 39 is a strain sent to our laboratory by Richard Moyer and is said to contain a mutant Collb factor which will allow 75 to replicate. I have used this strain to eliminate the likelihood that pathophysiological alterations observed during T5 infection of RM 43 are due to Collb-borne genetic determinants unrelated to the determinants necessary for abortive infection. There is a possibility, however, that our laboratory stock of what is identified as RM 39 no longer contains the plasmid. This would explain TS's ability to replicate in the strain, but would invalidate the interpretations of experiments involving RM 39.

As can be seen in Table 1, RM 33 does indeed produce a substance, thought to be colicin Ib, which inhibits growth of bacteria sensitive to colicin Ib. This is presumptive evidence that the strain contains the Collb factor. Since the presence of colicin Ib has not been risorously demonstrated, however, I thought it wise to demonstrate the plasmid on an ethidium bromide-cesium chloride gradient.

Labeled DNA was extracted from RM 42, RM 43, and RM 39. [<sup>14</sup>C]Labeled DNA from RM 42 was mixed with [<sup>2</sup>H]-labeled DNA from RM 43.
As can be seen in Figure 4a, DNA from RM 43 appeared in two bands, one
in the position characteristic of covalently closed, circular DNA
(plasmid DNA), the other in the position characteristic of nicked
circular DNA (E. col1 chromosome) (21). DNA extracted from RM 42,
however, banded in a single position characteristic of the E. col1
chromosome. A second tube, which was centrifuged concurrently, contained [<sup>2</sup>H]-labeled DNA from RM 43 and [<sup>2</sup>H]-labeled DNA from RM 39

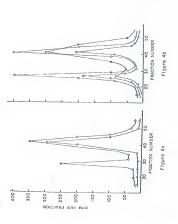
rom RM 42, RM 43, and RM 39.

OWA 10 WILL SEAR Labeled by proving in the presence of PATH towards of 87 39 was a labeled with PATH by proving in (11 City Per 11 Link) per 4 as of PATH by part of 11 City Per 4 as of PATH by PATH

O, RM 43 0NA (<sup>3</sup>H)

▲, RM 39 0NA (<sup>14</sup>C)

■, SV40 0NA (<sup>32</sup>P) . RM 42 DNA (14c)



(Fig. 4b). Additionally, this tube contained  $[^{32}P]$ -labeled SV40 DNA which is known to consist of both covalently closed, circular DNA and nicked, circular DNA (4). As before, two peaks appeared, each containing  $[^3H]$  counts of RN 43 DNA. These peaks were in positions identical to peaks containing  $[^{32}P]$  counts of SV40 DNA and  $[^{14}C]$  counts of RN 39 DNA. The results conclusively show that both RN 39 and RN 43 contain plasmid DNA.

### Confirmation that T5h12 Infections Begin Promptly

Studies using TSNI2" mutants have been performed to eliminate the likelihood that pathophysiological alterations observed during T5 infections of RM 43 are due to phage genetic determinants unrelated to the A3 gene function. If the TSNI2" phage were very slow to initiate infections in RM 43, normal bacterial physiological processes would be expected to continue in the TSNI2"-RM 43 suspension for some time. This could invalidate interpretations of the experiments using these mutants.

To confirm that TSh12<sup>2</sup> phage adsorb and initiate infections promptly, breakdown of host DNA, an event normally occurring in the first minutes of infection, was monitored. As can be seen in Figure 5, breakdown of prelabeled host DNA into acid-soluble fragments occur promptly after T5 wild-type or TSh12<sup>2</sup> infection or RM 42, RM 43, or RM 39. From these results, it is evident that TSh12<sup>2</sup> phage are able to normally adsorb to and initiate infection in RM 43.

### Amino Acid Accumulation in T5 and T5h12 Infections of RM 42, RM 43, and RM 39

In an attempt to clarify the relationship between the inhibition of RNA and protein synthesis and the membrane changes previously observed



RACTERIA <sup>6</sup>H(CP/H)/2.2 x 10<sup>9</sup> DMA was labeled by growing the cells in the presence of [34] thymidine (0.4 UCi per ml, 1 UCi per 50 ug of thymidine). The cells were spun, concentrated, infected, and rediluted in medium without radiolabeled thymidine. At times thereafter, 0.9 ml samples were removed and placed in was filtered over glass fiber filter precipitable counts were determined The number of acid-0.1 ml of 50% TCA. and washed.

### uninfected cells .

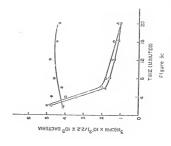
by liquid-scintillation counting.

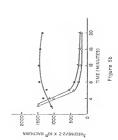
8

T5-infected cells









(19), and to more specifically define the membrane defects, I looked at accumulation of two marion acids. The transport systems of proline and glutamine are fairly well characterized (6,7), and both systems require an "energized" membrane. Proline requires membrane-bound transport proteins (still present when purified membrane vesicles are made), but does not require a high-energy phosphorylated intermediate. Glutamine, on the other hand, relies upon periplasmic binding proteins and needs ATP to energize its active transport. I wanted to see when, if at all, these uptake systems were inhibited during abortive infection. If they were inhibited, I wanted to know if they renained functional during infections involving h mutants of the phage or the plasmid.

In these experiments, aliquots of cells were removed at various times after infection and incubated with chloramphenicol for one minute -- a time sufficient to totally stop protein synthesis - prior to adding the labeled amino acid. The results, therefore, reflect only net uptake of the amino acid, and are not indicative of incorporation into proteins.

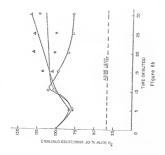
When wild-type TS infected any of our three bacterial strains, there was a slight drop in proline accumulation at 5 minutes after infection (Fig. 6a and Table 2). By 10 minutes into the infectious process, however, net uptake returned to uninfected levels in all cases, and continued to increase in both infected 8M 42 and infected 8M 39 (Collbh). In abortively infected 8M 30 (Collbh), however, there was a drastic reduction in the ability to accumulate proline between 10 and 15 minutes. If TSh12 phage infected 8M 43 (Collb)

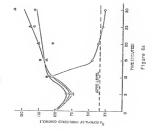
# Figure 6. Proline Accumulation in 60 Seconds by Infected RM 42, RM 43, and RM 39.

della were grown and frittered in synthetic medium. An the indicated in the after infection, samples were recoved and mixed with [34] provine and 0 seconds thereafter and if itered through glass fiber filters, infertier and if itered through glass fiber filters, infertier and infered through glass fiber filters, infertier and infered through glass fiber filters.

In the same part of the fife, so recommand in 6 seconds by control in the same part of it file. So recovered size in fractions of Ecological (2010), and 83 (2010). Fil. 9. 60 represents 1917-Tiffections of the same brief of the second size of the same filters in 1918 (2010).

♠, RM 42
 ♠, RM 43 (Collb)
 ♠, RM 39 (Collb h<sup>-</sup>)





TIME	TIME AFTER PHAGE	RM 42-T5wt vs RM 43-T5wt	-T5wt	VS R	43	-T5wt	(3)		RM 4	3-T	Swt	VS	RM 43-T5wt vs RM 39-T5wt	-T5w	t (3)		
ю	minutes	83 ±	2 :		78 +	+ 1			78	+1	1		74 +	+1			1
10	10 minutes	113 ± 15	15		106 ±	± 24			106	106 ± 24	54		109 ±	2			
15	15 minutes	123 ±	± 27	*	46	+ 7			46	+1	7	*	114 ±	26			
20	20 minutes	105 ±	19	*	37	9+1			37	+1	9	*	127 ±	155			
25	25 minutes	133 ±	32	*	30	1 7			30	+1	_	*	138 ±	+ 48			
30	30 minutes	132 ±	23	*	27	41			27	+1	LC)	*	163 ±	55			
NaN3	MaNg +uninfected cells	12 ±	co +1	-	4	4			14	+1	4		16 ±	00			
TIME	IME AFTER PHAGE	RM 43-T5h12 VS RM 43-T5wt	T5h12	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	20	43-T5	wt (3)	RM 42-T5h12 vs RM 43-T5h12 vs RM 39-T5h12	5h12	N N	₩.	43	T5h12	\ \s	RM 39-T	5h12	5
10	5 minutes	79 ± 10	10		78	78 ± 14		79 ± 16	9		1 "	80 + 6	9		83 +	=	1
10	TO minutes	÷ 96	9		82 ±	+ 27		104 ± 26	9		Ξ	112 ± 2	27		103 ±	19	
15	15 minutes	92 +	16	*	55	==		119 ± 3	31		Us.	± 76	10		107 ±	=	
20	20 minutes	83 ± 12	12	*	23	+ 7		103 ± 2	22		ω	+ 98	29	*	+1	36	
25	25 minutes	92 +	6	*	49	10		102 ± 2	25		-	+ 6/	+ 12	*	130 ±	26	
30	30 minutes	83 ±	6	*	46	6+1		124 ± 2	56	*	_	+1	78 ± 12		135 ±	30	
NaN3 +	NaN3 + uninfected	32 +	2		32	2		32 ± 2	23		2	1 52	12		44 ±	6	

indicates a difference between the 2 samples with a confidence level, p< 0.05 ( ) indicates a number of experiments done in each group

[34] Profine accumulation by infected cells was determined as outlined in WATERIALS AND METHODS. The results represent %'s of uptake, relative to that of uninfected control samples, in 60 seconds.

(Fig. 6b), there was only a slight reduction in net uptake as compared to that seen during infections of RM 42 or RM 39 (Collbh'). In comparing results observed during TShl2' infections of RM 42 and RM 43 (Collb) by Student's t-test, only the difference in values at 30 minutes was significant. This slight loss in net uptake in colicinogenic hosts was perhaps due to the 50% plating efficiency of the mutant phage on RM 43 (Collb). When TS wild-type and TShl2' infections of RM 43 (Collb) were compared directly, statistically significant differences were observed at all times after 10 minutes. In summary, the ability to accumulate proline was drastically reduced between 10 and 15 minutes in nonpermissive hosts. This inhibition was not observed when h mutations on either the phage or plasmid allowed productive infection to occur.

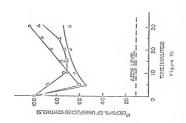
Similar results are seen when glutamine uptake is measured (Fig. 7 and Table 3). After observing a reduction in uptake ability at five minutes after T5 wild-type infections of any one of the three strains, we saw a gradual recovery in uptake ability during productive infections. When RM 43 (Collb) was the host, uptake ability fell progressively, and there was a statistically significant difference, as compared to infections of RM 42, by 15 minutes. Although the ID minute values were not significantly different, in some experiments there was indeed a large disparity. The mean ID-minute value of glutamine uptake in infected RM 43 (Collb) was lower than the value of infected RM 39 (Collbh). Infection of RM 43 (Collb) with TShl2° or 15 wild-type showed that the h mutation prevented the fall in glutamine uptake. The cell's ability to accumulate glutamine, then, as was the

Figure 7. Glutamine Accumulation in 90 Seconds by Infected RM 42, RM 43, and RM 39.

Coll sever grown and frienced at synchetic inadium. At the indicated ritters, samples were removed and inside title [16] glitamine (0.5 LLC) bear in [1.5 LLC] for mine]. J. Lift of the collection of the control of the collection of the Carlo o

●, RM 42 ○, RM 43 (Collb)

▲, RM 39 (Collb h<sup>-</sup>)



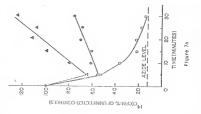


TABLE 3. Glutamine Accumulation (in 90 seconds) by Infected RM 42, RM 43, and RM 39

TIME	TIME AFTER PHAGE	RM 42-T5wt vs RM 43-T5wt	VS R	4		(4)	RM 4	13-TE	wt.	RM 43-T5wt vs RM 39-T5wt	-T5wt	(3)	
ın	minutes	54 ± 25		± 09	+ 11		57	+1	m	64	9		
10	10 minutes	61 ± 33		35	± 13		37	+1	6	+ 80 +	Ξ		
15	15 minutes	60 ± 30	*	21	=======================================		21	+1	12	100 ±			
20	20 minutes	69 ± 31	*	13	10 +		25	+1		112	36		
25	25 minutes	68 ± 45	*	17	10 +		14	+1			38		
30	30 minutes	75 ± 48	*	16	1 7		12	+1	*		122		
vaN3	NaN3 + uninfected cells	17 ± 17		15	ص +1		15	+1		22 -			
TIME	TIME AFTER PHAGE	RM 43-T5h12	2	至	vs RM 43-T5wt	(4)	RM 42-T5h12	8	RM 4	3-T5h12	8 >	RM 42-T5h12 VS RM 43-T5h12 VS RM 39-T5h12	112
ιΩ	5 minutes	65 ± 14		99	e +1		55	1	l	09		88	1
10	10 minutes	66 ± 21	*	38	1 16		64			74		7.1	
15	15 minutes	75 ± 16	*	24	12		73			76		73	
20	20 minutes	71 ± 19	*	25	1 15		89			85		74	
25	25 minutes	73 ± 28	*	2	1 10		77			93		78	
30	30 minutes	74 ± 28	*	9	co +1		68			104		96	
alv3	NaN3 + uninfected	12 ± 5		12	10		2			2			

( ) indicates the number of experiments done in each group

 $\lfloor^{1}6\zeta\rfloor$  Glutamine accumulation by infected cells was determined as outlined in MATERIALS AND METHODS. The results represent  $\mathbb{X}^{1}$ s of uptake, relative to that of uninfected control samples, in 90 seconds. indicates a difference between the 2 samples with confidence level, p< 0.05

case with proline uptake, was drastically reduced during abortive infection. This dysfunction was prevented by phage or plasmid mutations which also allow productive infection to proceed. There was a tendency for glutamine uptake to decline a bit earlier than proline uptake but the two uptake systems were not compared in the same experiment.

### Confirmation that Inhibited Proline and Glutamine Accumulation is Not Due Solely to Inhibited Protein Synthesis

One possibility is that the decreased net amino acid uptake is due solely to cessation of protein synthesis. There could, for example, be an accumulation of amino acids in TS-infected RM 43 after protein synthesis stops at 9 to 12 minutes after infection. This might limit net uptake of proline or alutamine from the medium.

I therefore treated uninfected or T5-infected cells with chloramphenicol 1 minute or 15 minutes prior to determining net uptake of proline or glutamine from the medium. Even 15 minutes after inhibition of protein synthesis with the antibiotic, there was no decrease in accumulation of either amino acid from the medium when glucose was the carbon source (Table 4). These results eliminate the likelihood that the decrease in net uptake of amino acids during abortive infection is due only to cessation of protein synthesis.

### α-Methylglucoside Accumulation in T5 and T5hl2 Infection of RM 42, RM 43, and RM 39

Since accumulation of either proline or glutamine requires an energized membrane, I decided to measure net uptake of a substance which is transproted via a group translocation reaction, and does not require membrane polarization. offs is a nometabolizable analogue of glucose taken into the cell using the phosphotransferase system

TABLE 4. Proline and Glutamine Accumulation in Uninfected and Infected RM 43 After 1 Minute or 15 Minutes of Incubation with Chloramphenicol

	Pro	Proline (3)	Glutamine (3)	ne (3)	7
	Uninfected Cells	5 Minutes After T5	Uninfected	5 Minutes After T5	
hloramphenicol for 1 Minute	970 ± 166	875 ± 52	1331 + 98	793 ± 94	
Aloramphenicol for 15 Minutes	940 ± 198	1033 ± 190	1719 ± 49	1047 ± 118	

## ( ) indicates the number of experiments done in each group

[24] Porline or [FL]Q platenie examplation as determined a sutifixed is MyERRIAR, Sp METHODS. Secoupt Matte, where indicated, chloremphenicol was allowed to inhibit protein sorbiests from 18 minutes prior to massuring examplation of the blacked minute acid. Results represent row spours accountable by approximately \$2.2 x 108 cells in 60 seconds (profilms) or in 50 seconds glutamine). and energy derived from phosphoenolpyruvate (57). I wanted to see if this transport system was functional in abortively infected cells.

Phage infection, whether productive or abortive, increased rather than decreased oNS accumulation (Fig. 8 and Table 5). By 5 minutes after infection, however, the increase was much greater in the abortive infection than it was in the productive infection. As was seen for proline or glutamine uptake, the absence of the normal phage or plasmid h gene product eliminated the effect. The augmented accumulation during abortive infection was inhibited by NaT, as is normal for transport systems energized by phosphoenolpyruvate (57), showing that the increased uptake was via the phosphotransferase system and not a new uptake system. After 10 minutes of infection in a non-permissive host, the increase in oNS accumulation began to decline, although the total uptake was still much greater than that during productive infection.

### Glucose Incorporation into Macromolecules in T5 and T5hl2- Infection of RM 42, RM 43, and RM 39

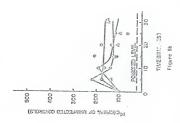
The rate of protein synthesis or nucleic acid synthesis measured by incorporation of radiolabeled precursors depends first upon the cells' ability to take up the precursor from the medium. Since the uptake of amino acids into the soluble pools of T5-infrected cells was severely depressed during abortive infection, it cannot be said that protein synthesis was necessarily inhibited. Since the glucose transport system appeared to remain functional, as measured by dMG uptake, we have looked for the incorporation of label from [<sup>14</sup>C]-glucose into acid-insoluble material [fig. 9].

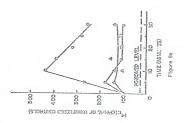
### α-Methylglucoside Accumulation in 90 Seconds by Infected RM 42, RM 43, and RM 39. Ffgure 8.

After a wown was most metected in systellate (medium in the the indicated After a second wash, intensity of a second wash, the elit syste exceptended they with 18 and of 10 all of P(C) and (10 LC) per mil. 184.cc] server monely has added to 0.5 in 0 for the clin suspension in Allouots were removed at 45 and 00 seconds, therefore, and were filtered through plass fiber filters. The results the new for the 90-second bulles, soperessed as a 2 of the amount taken up by invifected consolisity in the same paried of time. The filter fifteeting phage is Tout, whereas filt Fig. 8b, tt is Toni?

●, RM 42 ○, RM 43 (Collb)

▲, RM 39 (Collb h<sup>-</sup>)





(3)								RM 39-T5h12 (2)	137 ± 37	191 ± 37	124 ± 15	108 ± 2	99 ± 12	154 ± 20	
RM 43-T5wt vs RM 39-T5wt	± 18 * 140 ± 4	74 * 104 ± 31	85 * 131 ± 12	9 * 108 ± 15	48 * 113 ± 27	30 * 141 ± 46	10 18 ± 7	VS RM 43-T5h12 vs R	177 ± 59	167 ± 17	211 ± 130	180 ± 36	65 ± 13	157 ± 61	4 50
RM 43-T	254 ±	439 ±	392 ±	323 ±	282 ±	257 ±	25 +	RM 42-T5h12" vs.	219 ± 6	137 ± 19	112 ± 14	134 ± 24	118 ± 4	148 ± 15	4 4 4
5wt (4)	41	72	70	26	52	33	14	-T5wt (1)	245	354	313	313	228	260	0.1
VS RM 43-T	* 270 ±	* 426 ±	* 384 ±	* 343 ±	* 296 ±	* 261 ±	24 ±	" vs RM 43-T5vt							
RM 42-T5wt vs RM 43-T5wt	177 ± 40	140 ± 12	108 ± 19	107 ± 20	114 ± 18	100 ± 28	25 ± 7	RM 43-T5h12"	202	225	169	164	153	134	00
TIME AFTER PHAGE	5 minutes	10 minutes	15 minutes	20 minutes	25 minutes	30 minutes	NaNg and NaF + uninfected cells	IME AFTER PHAGE	5 minutes	10 minutes	15 minutes	20 minutes	25 minutes	30 minutes	MaN and Man .

indicates the number of experiments done in each group

The  $\mathbb{L}^{14}\mathbb{C}_j$  and accumulation by infected cells was determined as outlined in WATERIALS AND WETHODS. Tresults represent %'s of uptake, relative to that of uninfected control samples, in 90 seconds. indicates a difference between the 2 samples with a confidence level, p< 0.05

Glucose Incorporation into Acid-Insoluble Macromolecules in Uninfected and Infected RM 42, RM 43, and RM 39, Cells were grown and larfected in Christian Christian (145) follows with the common control of the co

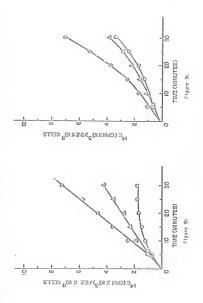
4°C (CPM X 10°3)/2.2 X 10<sup>8</sup> CELLS

0

- uninfected cells
- ○, T5-infected cells

  ▲, T5hl2<sup>-</sup>-infected cells





Cumulative incorporation of glucose into an insoluble form was inhibited in the abortively infected RM 43 (Collb) at about 10 minutes after infection (Fig. 9b). This was not the case during T5 infections of RM 42 or RM 39 (Collbh) (Fig. 9a and 9c), nor was it true of T5hl2<sup>-</sup> infections of RM 43 (Collb) (Fig. 9b). Since the glucose transport system remained operative for at least 30 minutes during abortive infection, it appeared that macromolecular synthesis per se was inhibited at about 10 minutes. This conclusion must still be regarded as tentative, however, since the results could be explained by leakage of intermediary metabolites of glucose. Further investigation of this problem may be warranted.

### Fluorescence Intensity of NPN During T5 and T5hi2- Infection of RM 42, RM 43, and RM 39

The results of the uptake studies suggested that membrane depolarization was occurring at about 10-12 minutes after T5 infection of Collb-containing hosts. If true, when cells are infected in the presence of RPN, the fluorescence intensity emitted should increase at about this time, since chemicals known to depolarize the bacterial membrane have this effect (44).

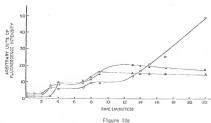
As can be seen in Fig. 10, when TS infects any of the 3 strains in the presence of NPM, there is an increase in fluorescence intensity at about 3 minutes after infection and another at about 6 minutes after infection. This biphasic effect has been observed previously (41) and is thought to reflect changes in the cell membrane at the times of first- and second-step DMA transfer. Data presented below are consistent with this interpretation.

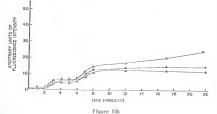
Figure 10. Fluorescence Intensity of N-phenyl-1naphthylamine during T5 and T5hl2<sup>-</sup> Infections of RM 42, RM 43, and RM 39.

Cells were grown, concentrated, and infected in synthetic medium. At time zero, the infected cells were put into presented growth medium containing the concentration of the conc

0, RM 42

○, RM 43 (Collb)
▲. RM 39 (Collb h)





Only in TS-infected RM 43 (Collb) is a third rise noted. The final increase in the fluorescence signal begins about 12 minutes after infection of the colicinogenic hosts, coinciding with the time when macromolecular synthesis ceases and uptake systems fail. Only the first two rises are seen after infection of RM 42 or RM 43 (Collb) by the TS host range mutant, TSh12<sup>-</sup>. The latter finding is consistent with the idea that the third rise in fluorescence yield is related to the abortive process.

### Potassium Efflux During T5 Infection of RM 42, RM 43, and RM 39

The third increase in fluorescence intensity during abortive infection suggests that membrane depolarization occurs. To collect further evidence of this, I decided to measure efflux of potassium fons during IS infection.

After preloading cells with <sup>42</sup>K, a portion was infected with T5, whereas another portion remained uninfected. Samples of each were taken at intervals. As can be seen in Table 6 and Figure I1, labeled potassium ions pass to the medium during the first 4 to 8 minutes of productive or abortive infection. Thereafter, however, efflux stops in infected RM 42 or RM 39. Efflux continues in the abortive infection, though, so that by 10 minutes after infection there is a marked difference between the cells which are productively or abortively infected as regards labeled potassium content.

### Attempts to Prevent Abortion of T5 Infection of Collb-Containing Cells

In several other systems where abrupt cessation of energyrequiring events occurs in conjunction with membrane alterations,

Figure 11. Potassium Efflux from T5-Infected RM 42, RM 43, and RM 39.

Cells were grown in the presence of radio-labeled potassium (0.1 mG iper ml, 0.18 mGi per mg of K), spun, washed, and infected or mock-infected. At time zero, the infected or mock-infected cells were resuspended in indicated intervals thereafter, 0.9 ml samples were removed, filtered over glass fiber filters, and the filters were washed. The amount of residual, intracellular labeled potassium was determined by liquid scintillation counting. The results infected cells, expressed as a 5 of the amount remaining in mock-infected cells taken at the same time point.

, RM 42 , RM 43 (Collb) A. RM 39 (Collb h<sup>-</sup>)

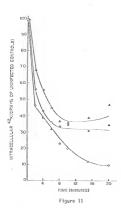


TABLE 6. Potassium Efflux From T5-Infected RM 42, RM 43, and RM 39

Minutes After infection	RM 42 (3)	RM 43 (3)	RM 39 (1)
2	56 ± 2	46 ± 27	68
4	43 + 10	39 ± 28	56
6	32 ± 7	36 ± 26	45
8	34 ± 8	.23 ± 12	37
10	*35 ± 7	*20 ± 8	36
15	*31 ± 9	*12 ± 9	39
20	*35 ± 11	*10 ± 3	47

<sup>( )</sup> indicates the number of experiments done in each group

BM 42, BM 43, and BM 39 were preloaded with  $^4$ Ck. At intervals, uninfected and infected cells were taken to determine the amount of potassium efflux. The results represent the amount  $^4$ Kr remaining inside infected cells, expressed as a  $^8$  of the amount remaining in uninfected cells taken at the same time point.

<sup>•</sup> Indicates a statistically significant difference, p. 0,05, between mean values for infected RM 42 and infected RM. 3. Since efflux from infected RM 39 was only measured in one experiment, statistical analysis was not used to compare these results with those obtained with infected RM 42 and RM 43.

means have been devised to prevent interruption of normal processes.

I decided to screen a variety of these treatments to determine if any
would be effective in allowing T5 to replicate in Collb-containing
cells.

DCCD is an inhibitor of membrane-bound ATP'ase (43), and has been used effectively in conjunction with high concentrations of magnesium and potassium to prevent colicin K-mediated cell death (56). Sucrose or polyamines, or high concentrations of either magnesium or calcium with low sodium concentrations have been effective in preventing abortion of T4-II mutant infections of  $\underline{E}$ ,  $\underline{coli}$  k-12 ( $\lambda$ ) (14).

Table 7 outlines my results. In no case was a treatment effective in circumventing abortive T5 infection, as determined by titering phage present 4 to 7 hours after infection. Since calcium is required for successful T5 replication (59, 77, 78), high calcium concentrations were also tested. These trials were similarly unsuccessful.

### Macromolecular Synthesis in T5 Wild-Type and T5Al Infection of RM 42, RM 43, and RM 39

It was my opinion that a previous report (45) suggesting that
early protein synthesis was necessary for abortive T5 infection was
inconclusive. Therefore, I used mutants of T5 to restudy this question.
The T5Al<sup>-</sup> phage mutants are enimently suited for this purpose. As
discussed in the INTRODUCTION, these mutants cannot produce any
class II or class III proteins, since the Al function is required for
second-step DNA transfer. Al<sup>-</sup> mutants are also unable to shut off
class I gene expression, another function controlled by the Al gene
(71). I have used two mutants, TSmm16d and TSmm127, each of which has
an amber mutation in the Al region (5).

TABLE 7. Attempts to Prevent Abortion of T5 Infection of Collb+ Hosts

Sacteria	Potassium	Calcium	Magnesium Sodium	Sodium	Sucrose DCCO	0000	Polyamine	Titer
		N- H						. III.
				4				/x
				+		+		3 × 1010/1
				+				108/11
				4		4		200
						٠		E/201 X
	,		+			+		1 x 108/m
	+		+	,				7 ~ 108/m
	+		+			+		100
					-			108/11
			+					2 × 0 × 0
								100 x 00
					٠			W/001 x 2
				+			cadaverine	7 × 100/m
			+		,	,	cadaverine	1 × 109/m
				+			avering	, 108/m
			+				averinge	109/m/
RM 43		0.5 mM		+			chemidine	108/11
			+				enormedeno	2 0 108/m
			-				ani n i i i a i i e	100
		1				,	1	3 × 100/m
		4 mM	+		+	,		6 × 10 <sup>8</sup> /m
N 43		A mM	+		+	+		1 × 108/m
M 43		A mM	+		,			0

Lolls were govern and infected as notalized in AMERIALS AND URFIGORS. The office of the MIERIALS AND MIERORY AND FIGURES of a first three were present at concentrations also indicated in AMERIALS AND MIERORY. At 2 p hours after infection, the phage were placed on a lawn of  $\underline{E}_{\rm c}$   $\underline{col}$  8 to fifteen the tites.

Figure 12 represents cumulative  $[^3k]$  uridine incorporation into TCA-precipitable material in infected bacteria, while Figure 13 shows the results of the analogous experiments with  $[^3k]$  tyrosine. Uptake of the labeled precursors and incorporation into macromolecules continue for at least 24 minutes after 804.2 is infected with either wild-type T5 or with an A1 $^-$  mutant. In the corresponding infections of 804.33 (Collb), however, incorporation of both uridine and tyrosine into macromolecules stops at 6 to 12 minutes after either mutant or wild-type phage is added. The possibility that this shut-off in 804.33 (Collb) is due to a property of the colicinogenic host unrelated to abortive infection is ruled out by the fact that incorporation of both substances in infected 804.39 (Collb h $^-$ ) continues for the duration of the experiments. From these experiments, it is evident that only class I (pre-early) gene products are necessary to induce the abortive cessation of RNA and protein synthesis.

### Proline, Glutamine, and aMG Accumulation in T5 Wild-Type and T5aml6d-Infected RN 42, RM 43, and RM 39

Previously, it was shown that decreased ability of host cells to accumulate proline and glutamine is characteristic of abortive infections, while enhancement of net uptake of aMS occurs. Experiments cooparing the ability of T5sinl6d-or wild-type T5-infected RM 43 (Collb) and RM 39 (Collb h<sup>-</sup>) to transport these three substances are shown (Fig. 14, 15, 16; Tables 8, 9, 10). The inhibition of proline and glutamine net uptake is the same whether a wild-type or an Al<sup>-</sup> mutant infect a non-permissive host. Likewise, the stimulation of aMG transport occurs when either Al<sup>-</sup> mutants or wild-type phage are used.

Uridine Incorporation into Acid-Uninfected and T5Al - Infected RM 42, RM 43, and RM 39. insoluble Macromolecules in

Cells were grown and infected it synthetic medium. [3H] Uridine synthetic medium.  $[^3H]$  Uridine (1 uCi per ml. 5 uCi per umole) on glass fiber filters, and the filters were washed. The amount of incorporated radioactivity were removed at the times and mixed 0.1 ml of cold 50% TCA. was added at time zero. the bacteria used were Fig. 12b represents obtained with RM 43 in Fig. 12c, RM 39 was determined by insoluble material ation counting. indicated of 0.9 ml

O, control, no infection

T5aml6d infection T5amH27 infection

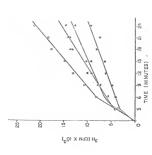
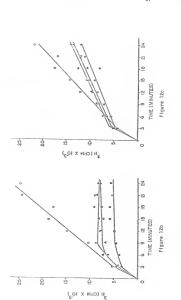


Figure 12a



Uninfected and TSA1-Infected RM 42, RM 43, and RM 39. insoluble Macromolecules in

Cells were grown and infected in synthetic medium. [3H] Tyrosine (1 µCi per ml, 7.2 µCi per µmole) was added at time zero. Samples insoluble material was recovered on glass fiber filters, and the times and mixed with Ac1d-'fg. 13a, the host was RM 42; n Fig. 13b, the host was RM 43 of 0.9 ml were removed at the amount of incorporated radioactivity was determined. In (Collb); in Fig. 13c, the was RM 39 (Collb h-). 0.1 ml of cold 50% TCA. Indicated

(CPS X 10<sup>2</sup>)

O, control, no infection

T5wt infection 

F5am16d infection [5amH27 infection 9



8 N z 2

12 22

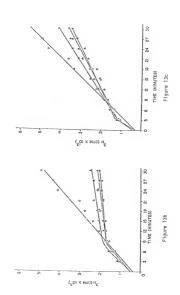
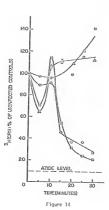


Figure 14. Proline Accumulation in 60 Seconds by T5A1-Infected RM 42, RM 43, and RM 39.

Cells were grown and infected in synthetic medium. At the indicated times after infection, samples were removed and instead with [24] prolline (1 pc) per ml, 25 pc) per mmole). Aliquots were removed at 30 seconds are only a count of the country of the country of the country of the amount cells is expressed as a % of the amount taken up by uninfected controls in the same period of time.

, T5am16d-infected RM 42

, T5wt-infected RM 43 (Collb)



66

TABLE 8. Proline Accumulation (in 60 seconds) by Infected RM 42, RM 43, and RM 39

RM 42-T5am16d vs RM 43-T5am16d vs RM 39-T5am16d(3) RM 43-T5am16d vs RM 43-T5wt(1)	64 ± 10 88 70	107 ± 26 87 115	112 ± 33 45 54	109 ± 25 40 31	121 ± 29 41 24	113 ± 22 32 21	* + 11
RM 43-T5am16d vs RM	89 ± 15	91 ± 4	46 ± 2 * 1	37 ± 13 * 1	37 ± 10 * 1	27 ± 9 * 1	+ 3
RM 42-T5am16d vs	97 ± 40	96 ± 24	* 31 = 011	* 8 + 66	* 6 = 911	142 ± 26 *	10 + 5
CONDITION	5 minutes after phage	10 minutes after phage	15 minutes after phage	20 minutes after phage	25 minutes after phage	30 minutes after phage	NaN2 + uninfected cells

( ) indicates the number of experiments done in each group

[34] Proline accumulation by infected cells was determined as outlined in MATERIALS AND WETHORS. The results represent %'s of uptake, relative to that of uninfected control samples, in 60 seconds. \* indicates a difference between the 2 samples with a confidence level, p <0.05

Figure 15. Glutamine Accumulation in 90 Seconds by T5A1 -Infected RM 42, RM 43, and RM 39.

Calls were grown and infected in synthetic medium. At the ingicated times, samples were removed and mixed with [46] alutanine (0.5 pCl per ml. 5 pCl per mole). At 30, 60, and 90 seconds thereafter, aliquous were removed and filtered through glass fiber filters. The results here are for the 90-second pulses, expressed as a % of the amount taken up by uninfected controls in the same period of time.

), T5am16d-infected RM 42

O. T5am16d-infected RM 43 (Collb)

A , T5am16d-infected RM 39 (Collb h")

. T5wt-infected RM 43 (Collb)

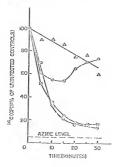


TABLE 9. Glutamine Accumulation (in 90 seconds) by Infected RM 42, RM 43, and RM 39

CONDITION	RM 42-T5am16d v	RM 42-T5am16d vs RM 43-T5am16d (	(3) RM 43-T5am16d vs RM 43-T5wt	M 43-T5wt (3)
5 minutes after phage	61 ± 17	70 ± 24	70 ± 24	52 ± 20
10 minutes after phage	55 ± 12 *	33 ± 10	33 ± 10	35 ± 2
15 minutes after phage	54 ± 11 *	21 ± 2	21 ± 2	24 ± 7
20 minutes after phage	* 65 ± 24 *	16 ± 5	16 ± 5	18 ± 5
25 minutes after phage	71 ± 31 *	16 ± 5	16 ± 5	17 ± 4
30 minutes after phage	74 ± 36 *	14 ± 5	14 ± 5	17 ± 6
MaNg + uninfected cells	7 ± 2	5 ± 4	5 ± 4	
CONDITION	RM 39-T5am16d v	RM 39-T5am16d vs RM 43-T5 16d (	(2)	
5 minutes after phage	8 ‡ 06	82 ± 15		
10 minutes after phage	* 9 7 06	31 ± 13		
15 minutes after phage	* 1 + 98	20 ± 2		
20 minutes after phage	* 17 + 17 *	13 + 2		
25 minutes after phage	77 ± 2 *	19 ‡ 0		
30 minutes after phage	* 8 = 09	16 ± 5		
NaN <sub>3</sub> + uninfected cells	5 + 4	2 ± 2		

\* indicates a difference between the 2 samples with a confidence level, p < 0.05 ( ) indicates the number of experiments done in each group

 ${}^{14}{}^{\rm C}$  Glutamine accumulation by infected cells was determined as outlined in WWEBIALS AND WETHODS. The results represent percentages of uptake, relative to that of uninfected control samples, in 90

Figure 16. α-Methylglucoside Accumulation in 90 Seconds by T5A1--Infected RM 42, RM 43, and RM 39.

, T5am16d-infected RM 42

O, T5am16d-infected RM 43 (Collb)

A, T5am16d-infected RM 39 (Collb h)

III. T5wt-infected RM 43 (Collb)

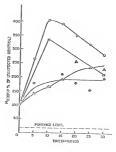


TABLE 10. a-Methylglucoside Accumulation (in 90 seconds) by Infected RM 42, RM 43, and RM 39

CONDITION	RM 42-T5am16d	RM 42-T5am16d vs RM 43-T5am16d (4)	RM 43-T5am16d vs RM 43-T5wt (1)	T5wt (1
5 minutes after phage	180 ± 23	* 296 ± 67	328	
10 minutes after phage	165 ± 41	* 429 ± 89	393 331	
15 minutes after phage	212 ± 27	* 361 ± 50	225	
20 minutes after phage	181 ± 60	* 348 ± 54	300	
25 minutes after phage	157 ± 45	* 320 ± 69	213 212	
30 minutes after phage	198 ± 54	256 ± 77	165	
NaN3 + NaF + uninfected cells	19 ± 7	19 ± 10		
COMDITION	RM 39-T5am16d	RM 39-T5am16d vs RM 43-T5am16d (3)		
5 minutes after phage	143 ± 8	* 267 ± 42		
10 minutes after phage	165 ± 21	* 405 ± 92		
15 minutes after phage	194 ± 37	* 393 ± 49		
20 minutes after phage	259 ± 72	352 ± 66		
25 minutes after phage	239 ± 38	320 ± 85		
30 minutes after phage	234 ± 21	283 ± 70		
NaN3 + NaF + uninfected cells	10 ± 8	17 ± 10		

 $[^{14}\mathrm{G}]$  aNG accumulation by infected cells was determined as outlined in MATERIALS AND NETHODS. The results represent %'s of uptake, relative to that of uninfected control samples, in 90 seconds. \* indicates a difference between the 2 samples with a confidence level, p< 0.05 ( ) indicates the number of experiments done in each group

# Fluorescence of Membrane-Bound NPN During T5Al Infections

When TSam16d infects RM 42, RM 43, or RM 39 in the presence of NPN, there is an increase in fluorescence intensity at about three minutes after infection but no increase at about 6 minutes (Fig.17). Since the mutant is deficient in second-step DNA transfer, this is consistent with Hantke and Braun's idea that the second increase in fluorescence intensity reflects membrane alterations related to second-step DNA transfer (41).

that is evident, however, is the marked increase in fluorescence intensity at about 10 to 12 minutes only occurring after infection of RM 43. This is a pattern similar to that found after TS wild-type infection of the Collb\* colls.

# Potassium Efflux During T5aml6d Infections of RM 43

Cells were preloaded with radiolabeled potassium ions as described above. As can be seen in Table II and Fig. 18, the pattern of ionic efflux in Tsaml6d-infected RM 43 is similar to that during TS wild-type infection of RM 43. After plateauing early after infection, the numbers of residual intracellular counts falls rapidly beginning at about 8 to 10 minutes in each case. The reason for the greater early retention of preloaded ions in the TS wild-type-infected cells is unknown. These figures are much higher than those obtained in other experiments (Table 6). Since the amount of initial efflux is very dependent upon multiplicity of infection (94) and since the data in Tables 6 and II were derived on different days, it might be that the multiplicities of infection were not comparable. If so, however, this was inadvertent. Nonetheless, if comparing the patterns of efflux seen

Figure 17. Fluorescence Intensity of N-pheny)-1naphthylamine During T5Al Infections of RM 42, RM 43, and RM 39.

Cells were grown, concentrated, and infected in synthetic medium. At time zero, the infected cells were put into prewarmed growth medium containing the fluorescence intensity was recorded in arbitrary units using a scanning fluorimeter.

♠ , RM 42♠ , RM 43 (Collb)♠ , RM 39 (Collb h<sup>-</sup>)

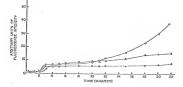


TABLE 11. Potassium Efflux from T5A1"-Infected RM 42 and RM 43

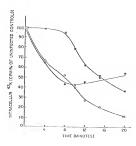
Minutes After Infection	RM 42-T5 <u>am</u> 16d	RM 43-T5 <u>am</u> 16d	RM 43-T5wt
4	65	67-55	99
8	43	52-48	95
10	42	40-33	79
12	46	27-29	62
15	51	21-17	51
20	55	11-9	37

80.42, 80.43, and 80.39 were preloaded with  $^{4}$ CK. At intervals, uninferected cells were taken to determine the amount of potassium efflux. The results represent the amount of  $^{4}$ CK remaining inside inferected cells, expressed as  $^{3}$  of the point. Leakage from Unfected cells taken at the same time point. Leakage from Unfected  $^{4}$ R4 Shame measured during the trials.

Figure 18. Potassium Efflux from TSA1 - Infected RM 42 and RM 43.

Calls were grown in the presence of radiolabeled potassium, spun, washed, and infected or mock-infected. At time zero, the infected or mock-infected cells were resuspended in medfum without he radiolabel. At the indicated intervals thereafter, 0.9 all samples were falled to the control of t

- , T5am16d-infected RM 42
- (Collb) T5aml6d-infected RM 43
- M, T5wt-infected RM 43 (Collb)



during T5 wild-type or T5aml6d infection of RM 43 to the efflux seen after T5aml6d infection of RM 42, it is apparent that the initial decline in residual counts during infection of RM 42 plateaus at about 8 minutes after infection. This is not true during infection of RM 43, wherein ionic efflux is marked beyond 10 minutes after infection.

### Absence of Host DNA Breakdown During T5am16d or T5am127 Infection

To confirm the identity of TS<sub>801</sub>[6d and TS<sub>801</sub>[27 nutants, a number of studies were performed. As can be seen in Table 1, these mutants do not plate efficiently unless the strain has suppressor activity. I have also tested these mutants for their ability to break down host DNA into acid-soluble fragments. This is the function of the Al polypeptide, and should be lacking in Al<sup>-</sup> mutants (62).

EM 42, EM 43, and EM 39 were grown in the presence of [3H] thymidine as described in MATERIALS ADD METHODS. As seen in Fig. 19, host DNA is not degraded to acid-soluble material after infection by TSA1 mutants, confirming the lack of production of a functional Al polypeptide.

## Gel Analysis of Phage Proteins

It was suggested that RM 43 (Collb) could have an <u>amber</u> suppressor present on the plasmid, invalidating any conclusions regarding infection of these cells with <u>amber</u> mutants. To show that this was not the case, by confirming that class II (early) or class III (late) proteins are not nade in Al<sup>-</sup>-infected, Collb<sup>+</sup> cells, we pulse labeled proteins synthesized from 1 to 6 minutes, 6 to 11 minutes, or 11 to 16 minutes after TS<u>aml</u>6d infections of the colicinogenic hosts (RM 43). On SDS-polyacrylamide gels, we compared these samples with those of TS<u>aml</u>6d

Absence of Host DNA Breakdown During T541 - Infections of RN 42, RM 43, and RM 39.

Figure 19.

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DNA was labeled by growing the cells in the presence of [54] thymidine (0.4 uC; per mg.). I LC! per 50 up on thymidine). The cells were spun, contravalue). Ifquid-scintillation he numbers of acid-precipitable count centrated, infected, and rediluted in nedium lacking radiolabeled thymidine. was filtere nost 1c RM 43 50% TCA. Of this, 0.4 ml was filter over glass fiber filters and washed. were removed and placed in 0.1 ml of the host is At times thereafter, 0.9 ml samples vere determined by RM 42; in Fig. 19b, (Collb), whereas in (Collb hcounting. e pM 3g

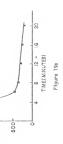
). uninfected cells

1000

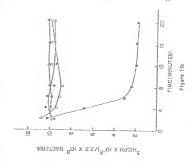
3H(CPM)/2.2 X108

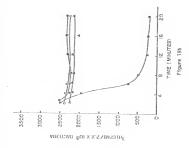
T5-infected cells n T5am16d-infected cells









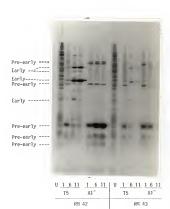


infections of RM 42, and with T5 wild-type infections of both strains.
Only class I (pre-early) proteins were seen during Al<sup>-</sup> infections of
either host strain (Fig. 20).

Figure 20. Gel Analysis of Phage-Induced Proteins During T5 and T5Al- Infections of RM 42 and RM 43.

Cells were grown and infrected in a synthetic modium. At the times indicated, RM 42 or RM 43 (Collb) infected with either 15 or 15m16d were tabeled with 1 uci per mil or a [14c] amino acid later, and the cells were chilled. Then, they were centriqued, washed and resuspended in 1/10th volume of electrophoresis buffer and boiled for 5 minutes. Electrophoresis or 20 µ1 at 25 minutes. The company of the cells were child to the cells were contributed to the cells were contributed and the cells were contributed to the cells were cells with the cells were cells were cells with the cells were cells with the cells were cells were cells were cells with the cells were cells were cells with the cells were cells with the cells were cells were cells were cells were cells with the cells were c

The numbers across the bottom indicate the time after infection when the pulse began. The proteins were called pre-early or early according to their time of appearance (70).



#### DISCUSSION

It has been known for more than 10 years that T5 is unable to replicate in hosts containing the colicin 1b factor (80, 97). Very little is known, however, about the mechanism whereby phage development is inhibited. Originally, no class II (early) or class III (late) proteins or RNA was seen on polyacrylamide gels. Because of this, it was hypothesized that a class-specific transcriptional block occurred (79). Later, though, it was found that some class II (early) proteins do actually appear. Additionally, functional RNA polymerase can be recovered from abortively infected cells (99), and no changes in the DNA .msplate are found that explain the abortive infection (45, 89). Thus, there seems to be no evidence to implicate a primary transcriptional or translational dysfunction.

It seems more plausible to suggest that a generalized cellular dysfunction is the cause. During abortive infection, there is abrupt, simultaneous cessation of both transcription and translation, and there are numerous other concurrent physiological alterations not easily explained by specific-site inhibition. As membrane defects are thought to play a key role in other abortive systems, I decided to see if changes in membrane function during T5 infections of Collb<sup>+</sup> hosts could underlie the abortive process.

Previously, others in Donna Duckworth's lab have reported that uptake of thio-G-methyl-D-galactoside (TMG), a nonmetabolizable lactose analogue taken up by an ATP-dependent, active transport mechanism (104) is inhibited during abortive infection (19). In the present study, I sought to further define the membrane's functional defects by looking at uptake of three additional substances -- proline, glutamine, and oNG -- each of which is taken up by a different mechanism (reviewed in 102).

Initially, however, I wented to define the abortive system in our laboratory. In agreement with the results reported by others (78), incorporation of radiolabeled uridine into TCA-insoluble macromolecules was found to stop 9 to 12 minutes after 15 infection of cells containing the Collb factor. This was the same time at which cessation of tyrosine and proline incorporation into acid-insoluble macromolecules occurred during abortive infection. Since I wished to define physiological alterations directly related to this abrupt interruption of the infectious process, I looked at changes occurring within the first 30 minutes after infection.

During abortive infection glutamine accumulation is inhibited, beginning to decline by 10 minutes after infection. Since the active transport of glutamine is an ATP-dependent process requiring periplasmic binding proteins (6, 7), decreased uptake ability might be due to decreased available ATP, loss of periplasmic binding proteins, or marked permeability changes which prevent concentration of the substance. The last of these explanations probably cannot totally explain the data, since at a time when glutamine accumulation is markedly depressed, aMG accumulation is three-to four-fold greater than that in uninfected cells. Regarding the loss of binding proteins, the inner membranes of abortively infected cells do not become sensitive

to SDS-induced lysis until more than 20 minutes after infection (18), so it is unlikely that the outer membrane integrity is destroyed to an extent necessary for periplasmic proteins to leak by 10 minutes after infection. The most likely explanation for the inhibition of glutamine uptake is that adequate energy is no longer available.

Net uptake of proline decreases during abortive infection at about the same time, or slightly later than the decline of glutamine accumulation. Proline uptake, unlike that of glutamine, does not require perfolasmic binding proteins (6, 7). Even isolated membrane vesicles are capable of proline uptake, indicating that components of the uptake system are bound firmly to the membrane (reviewed in 102). Nonetheless, proline uptake is similar to glutamine uptake in that it requires an "energized membrane." Invoking the same argument against warked membrane permeability changes by 10 to 15 minutes after infection, I think the most likely reason for decreased proline accumulation is also membrane demergization.

By membrane deenergization, I refer to loss of the transmembranal electrochemical gradient normally present (73). Since ions at low concentration obey the gas laws, this gradient can be expressed as:

$$\Delta \ \overline{\mu}_{\text{H+}} = \Delta \Psi - \frac{2.3 \text{RT}}{F} \ \Delta \text{pH,}$$

where  $\Delta F_{H+}$  equals the electrochemical proton gradient,  $\Delta Y$  represents electrical potential difference, R is the gas constant (8.3 joules per Kelvin degree), T equals the temperature in Kelvin degrees, F is the faraday (96,500 coulombs), and  $\Delta PH$  means the proton gradient. It is thought that a normal bacterium has a transmembranal electrical potential of 75 mV (84) to 140 mV (40), but at PH's near 7,  $\Delta PH$  is

very small (84, 88). Therefore, under conditions used in the proline and glutamine uptake experiments, loss of membrane energization would be equivalent to loss of ionic polarization.

If decreases of proline and glutamine accumulation do indeed result from membrane deenergization during abortive infection, the prediction is that loss of ionic polarization should occur at the same time.

This, in fact, has been shown herein, at least for the case of a major intracellular cation, potassium. Efflux of preloaded potassium from abortively infected cells becomes significantly greater than efflux from productively infected cells at about 10 minutes after infection.

Another prediction which is based on the assumption that the membrane is deenergized is that the fluorescence intensity omitted by NPN should increase dramatically during abortive infection. This change in fluorescence signal is observed when bacteria are treated with substances, such as derivatives of carbonyl cyanide phenylhydrazone. known to dissipate the high energy state of membranes (44). Since this lipophilic probe is neutral at physiological pH, it should not respond merely to changes in transmembranal potential (81). Rather, the rise in intensity is thought to occur due to structural changes in the outer membrane that are secondary to membranal deenergization (44). The structural changes in the outer membrane allow more NPN to bind to the inner membrane. Since the fluorescence intensity emitted by NPN increases directly as its environment becomes more hydrophobic (Leonard Rosenberg, personal communication), the observed increase is consistent with the interpretation that more of the probe moves into the lipid phase of the membrane. How or why it happens

was not investigated in the current study, but the predicted fluorescence changes did, in fact, coincide with the time when membrane depolarization is thought to occur in abortive infection.

Since binding-protein transport, represented by glutamine uptake, and membrane-bound transport, exemplified by proline uptake (reviewed in 102) were both inhibited, I decided to see if a substance taken up by group translocation was similarly affected. and is a nonmetabolizable glucose analogue taken into the cell by the phosphotransferase system (57). As the sugar is taken into the cell it is phosphorylated using phosphoenolpyruvate as its primary source of the phosphate group. At first, it seemed surprising that I found and accumulation was stimulated during abortive infection. However, this result is to be expected if the bacterial membrane becomes deenergized (Hans Kornberg, personal communication). In the absence of an energy-requiring dephosphorylating reaction, and becomes trapped within the cell as its phosphorylated derivative (49, 52). In fact, within a wide range of concentrations, dinitrophenol or azide causesa marked stimulation of any of the concentrations, dinitrophenol or azide causesa marked stimulation of any of the concentrations, dinitrophenol or azide causesa marked stimulation of any of the concentrations, dinitrophenol or azide causesa marked stimulation of

In all cases, the pathophysiological alterations indicative of membrane depolarization occur only during abortive infection. When the infection is productive because of plasmid-borne or phage-borne mutations, uptake systems function as in normal T5 infections of Collobosts, and neither the pronounced potassium leakage nor the abnormal fluorescence pattern is seen. It appears likely, therefore, that the membrane alterations are due to genetic determinants on the phage genome or plasmid DNA at those loci which also produce cessation of the infectious process.

The abortive pattern of pathophysiological alterations occurs. however, when Collb+ cells are infected with mutant phage deficient in second-step DNA transfer. The identity of the Al mutants used in our laboratory has been confirmed previously (29). I have also confirmed the mutant's inability to destroy the host genome, a known Al function (62). Furthermore, gel analysis of proteins synthesized during Al infections confirms the absence of early and late proteins. These data are strong evidence that only pre-early phage genes are required for the abortive response. They also indicate that the shutdown of phage gene expression is not the result of a class-specific transcriptional or translational defect, since the cessation of macromolecular synthesis during abortive infection usually occurs after early gene expression has begun (45, also see Fig 20 of this dissertation). Stated another way, the mechanism operable in shutting off the T5 replicative cycle does so at 10 to 12 minutes after infection, regardless of whether pre-early or early proteins are being synthesized at that time.

The evidence against a specific-site block and the data indicative of membrane depolarization strongly suggest that the mechanism leading to the abortive response is quite similar to the killing action of phage ghosts and to the bactericidal action of colicin proteins El, K, Ia, and Ib (66). Osmotically shocked T-even phage lose their DNA and their infectivity, but the empty protein shells retain the capacity to kill the host cell (47,48). Within two minutes, these "ghosts" inhibit DNA, RNA, and protein synthesis (27). Also quite early, uptake of OL-leucine and nucleic acid precursors (27), as well as the

uptake of β-galactosides (103), is diminished. Phosphorylated compounds including ATP, UTP, UDP, UPP, α-MG phosphate, and thio-β-methyl-galactoside phosphate leak from ghost-treated cells (30,48). Yet α-nitrophenylgalactoside (ONPG), carbamyl phosphate, or ATP entry is not embanced (30) indicating a peculiar sort of one-way permability defect. Additionally, ghost preparations contain some factor which causes a variable amount of cell lysis (47), but this lysis can be prevented by 0.05 M spermidine without influencing cell killing (D. Duckworth, unpublished data, cited in 28). Thus, phage ghosts inhibit macromolecular synthesis, inhibit active transport systems, cause "excretion" of at least some phosphorylated compounds, and cause a certain amount of cell lysis.

Similar actions are observed when sensitive bacteria are treated with colicin E1, K, Ia, or Ib -- collectively representing a group of proteins which are produced by plasmid-containing Enterobacteria and which seem to kill bacteria by the same (or similar) mechanism(s) (reviewed in 64). These proteins, for example, inhibit DNA, RNA, and protein synthesis (63,82). They also inhibit uptake of several amino acids (Gilchrist & Konisky, unpublished data, cited in 85,65; J. P. Kabat, cited in 86), of 8-galactosides (36, Gilchrist and Konisky, unpublished data cited in 55), and of potassium (Gilchrist & Konisky, unpublished data, cited in 55,101), rubidium (101), magnesium, and cobaltous ions (67). Colicins accelerate loss of preaccumulated potassium (Gilchrist & Konisky, unpublished data, cited in 55,101), magnesium, and cobalt ions (67) -- a change unlike that due to energy poisons (93) -- probably indicating a permeability defect. Also,

they cause cells to lose phosphorylated compounds (37), sugars, and amino acids (30, Gilchrist & Konisky, umpublished data, cited in 55). The membrane lipid and protein composition of treated cells is altered (16,17,18,53,90) and, under some conditions, the cells lyse (17). The lysis does not occur in minimal medium (67). Further, the rate of ONPG hydrolysis is unchanged (36), ATP is not found free in the medium (35), and a-MG uptake is augmented (52). Therefore, permeability to, or excretion of, various substances seems to be selective. In summary, physiological changes induced by ghosts and by colicins El, K, Ia, and Ib are quite similar.

This group of colicins is thought to act by forming ion channels (91). The evidence for this is derived from in vitro studies with phospholipid bilayers. Voltage-dependent, ion-permeable channels are introduced into bilayers by purified colicin preparations. Other data are consistent with this proposal. (1) Fluorescent dye probes indicate membrane deenergization (44,85), and the electrical transmembrane gradient is dissipated (100). (2) The decreased ATP level, characteristic after colicin treatment, is prevented in colicin Elor colicin K-treated cells by chemically or genetically inducing loss of membrane-bound ATP'ase activity (86). The inference is that the ATP'ase-deficient cells are unable to exhaust ATP supplies in what would be a futile effort to reestablish membrane polarity. (3) When ATP supplies are maintained in this way, macromolecular synthesis continues at a substantial rate (75), but transport activities are not improved. The idea arising from these observations is that cessation of macromolecular synthesis is secondary to the ATP deficit. However,

the membrane depolarization is not corrected, and therefore, active transport systems are still impaired. (4)  $\mathrm{AiP}^2$  as-deficient strains, when grown in glucose medium with high  $\mathrm{Hg}^{\pm}$  and  $\mathrm{K}^{\pm}$  concentrations, remain viable in the presence of colicin K or El (56). Under these conditions, essential intracellular cation concentrations are maintained, and the cell can continue metabolic functions. Since physiological studies completed thus far indicate numerous similarities among abortive T5 infections, phage ghost action, and colicin action, it might be that they all act by a mechanism somewhat similar to this.

Recently it has been proposed that T5 and BF23 infectious processes halted by the colicin Ib protein itself (D. J. McCorquodale. et al., submitted to J. Virol.; D. J. McCorquodale, personal communication). According to the model, the pre-early A3 gene product inactivates an immunity protein, which normally protects the bacterium from the colicin it produces. Abortive infection should not occur if the Collb plasmid is mutated such that the colicin protein is not produced, nor should it occur if the immunity protein is altered in such a way that it cannot be bound by the A3 protein but that it can still prevent the bactericidal action of the colicin protein. The infectious process should likewise proceed unhindered if there are alterations at the target site of the colicin protein or in blochemical pathways required for expression of the colicin's lethality. Furthermore, according to the model, other abortive systems such as T7 infection of F-containing E. coli and T4rII mutant infection of λ lysogens can be similarly explained. In each case, the hypothesis is that a potentially lethal protein encoded on the extrachromosomal

element (42) is activated by the infection -- leading to the cessation
of the infectious process before progeny appear.

This model, though promising, is currently based only on circum-

stantial evidence. Although an immunity protein for colicin E3 has been isolated (51), no direct evidence for the existence of a colicin Ib immunity protein has been described. Secondly, some permissive hosts bearing plasmid mutations have been found to lack the ability to produce the colicin protein (S. S. Tung, cited by D. J. McCorquodale), while other permissive strains with mutant plasmids do produce colicin (D. J. McCorquodale, personal communication). This does suggest that both the colicin and an immunity protein are involved in abortive infections, but the mutant strains have not been characterized well enough to say this with any certainty. Thirdly, there is only a weak suggestion that the chromosomal loci, cmrA and cmrB, involved in abortive infection are also the loci coding for the colicin Ib target. The evidence cited is that cmrA and cmrB map close to trkA and trkB, loci involved in potassium transport (33). Also, the toll gene, which confers tolerance to colicin Ib (15), maps close to another locus. trkC, involved in potassium transport (33). From these data, the hypothesis is that the cmrA, cmrB, and toll loci are identical to trkA, trkB, and trkC, respectively. Beyond this, it must be assumed that the potassium transport system is the target of colicin Ib. Fourthly, the comparison of the Collb system with other abortive infections cannot be as direct as is suggested by the model. For example, in the T4rII mutant system, the lack of a functional rll protein contributes to the abortive infection, whereas the presence of the A3 gene product is necessary for abortive T5 infection.

Nonetheless, the model is useful as a working hypothesis, as many testable predictions can be made from it. It should be possible to isolate a colicin Ib immunity protein, for example. Further, it should be possible to demonstrate an immunity protein-colicin Ib complex, to which the A3 phage gene product should bind. The addition of the A3 gene product should release a form of colicin Ib lethal for strains normally immune to, but not resistant to, the bactericidal action. Also, the prediction is that cmrA and cmrB mutants should be resistant to colicin Ib and should have defects in potassium transport. Importantly, strains with trkA, trkB, and toll mutations which have received the Collb plasmid should be permissive hosts for T5. Finally, it might be possible to find ionic conditions or membranestabilizing conditions under which abortive infection is prevented. Thus far, however, I have unsuccessfully tried to circumvent abortive infection using high concentrations of potassium, magnesium, calcium, alone or in combination; stabilizing the membrane with sucrose or polyamines have similarly failed to affect abortion. It is interesting in this regard, however, that ATP'ase inhibition, combined with high cation concentrations in the medium, was ineffective in preventing colicin Ib-induced cell death (56).

Another approach which holds great promise to understanding the role of the plasmid is restriction fragment analysis (64,95). EcoRI fragments of Collb, for example, could be sized and ordered. Then, individual fragments could be spliced to carrier plasmids, and the finerae placed into suitable Collb strains. The functions of the various fragments could then be ascertained. A modification of this

would be to determine the ability of the various chimeric plasmids to complement Collb factor mutants. In this way, genes controlling particular functions can be mapped.

In summary, evidence has been shown which indicates that membrane depolarization occurs at about the same as cessation of macromolecular synthesis during abortive T5 infection. Only the pre-early phage genes are necessary to elicit the same pattern of responses. No conclusive evidence exists to link the membrane depolarization and the interruption of the infectious process in a cause-effect relationship. Monetheless, the results do suggest a marked similarity among abortive T5 infection, the cell killing of phage shosts, and the bactericidal action of certain colicin proteins. The data presented here are consistent with a recently proposed model, which hypothesizes that the colicin Ib protein is in fact directly responsible for the abortive infection.

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Jerry Glenn was born on January 13, 1951, in Spangler, Pennsylvania. He attended public schools in that state and was graduated from Bellefonte High School in 1968. Thereafter, he enrolled in a five-year cooperative program in medicine offered jointly by The Pennsylvania State University and Jefferson Medical College of Philadelphia. The Bachelor of Science degree was awarded to him by Penn State in 1971, and the Doctor of Medicine degree was granted by Jefferson in 1973. In July of 1973, he began surgical training at the University of Florida Medical Center. He started graduate work in the Department of Immunology and Medical Microbiology two years later, in 1975, and received a Research Service Award (5 F32 AI-05296) from the National Institute of Allergy and Infectious Diseases in 1976. He married Judith McKean on December 14, 1978. After receiving his Ph.D. in June of 1979, he resumed surgical training at the University of Florida

I certify that I have read this study and that in my opinion it conforms to acceptable standards of scholarly presentation and is fully adequate, in scope and quality, as a dissertation for the degree of Doctor of Philosophy.

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